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<110> CANFIELD, William

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Asn Gly Gln Ile Pro Ser Trp Leu Asp Leu Ser Tyr Glu Arg Val Thr
35 40 45

Val Val Pro His Glu Val Leu Ala Pro Asp Pro Asp Gln Leu Pro Thr
50 55 60

Phe Ser Ser Ser Ala Ile Glu Thr Phe Leu His Arg Ile Pro Lys Leu
65 70 75 80

Ser Lys Arg Phe Leu Tyr Leu Asn Asp Asp Ile Phe Leu Gly Ala Pro
85 90 95

Leu Tyr Pro Glu Asp Leu Tyr Thr Glu Ala Glu Gly Val Arg Val Tyr
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Gln Ala Trp Met Val Pro Gly Cys Ala Leu Asp Cys Pro Trp Thr Tyr
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Ile Gly Asp Gly Ala Cys Asp Arg His Cys Asn Ile Asp Ala Cys Gln
130 135 140

Phe Asp Gly Gly Asp Cys Ser Glu Thr Gly Pro Ala Ser Asp Ala His
145 150 155 160

Val Ile Pro Pro Ser Lys Glu Val Leu Glu Val Gln Pro Ala Ala Val
165 170 175

Pro Gln Ser Arg Val His Arg Phe Pro Gln Met Gly Leu Gln Lys Leu
180 185 190

Phe Arg Arg Ser Ser Ala Asn Phe Lys Asp Val Met Arg His Arg Asn
195 200 205

Val Ser Thr Leu Lys Glu Leu Arg Arg Ile Val Glu Arg Phe Asn Lys
210 215 220

Ala Lys Leu Met Ser Leu Asn Pro Glu Leu Glu Thr Ser Ser Ser Glu
225 230 235 240

Pro Gln Thr Thr Gln Arg His Gly Leu Arg Lys Glu Asp Phe Lys Ser
245 250 255

Ser Thr Asp Ile Tyr Ser His Ser Leu Ile Ala Thr Asn Met Leu Leu
260 265 270

Asn Arg Ala Tyr Gly Phe Lys Ala Arg His Val Leu Ala His Val Gly
275 280 285

Phe Leu Ile Asp Lys Asp Ile Val Glu Ala Met Gln Arg Arg Phe His
290 295 300

Gln Gln Ile Leu Asp Thr Ala His Gln Arg Phe Arg Ala Pro Thr Asp
305 310 315 320

Leu Gln Tyr Ala Phe Ala Tyr Tyr Ser Phe Leu Met Ser Glu Thr Lys
325 330 335

Val Met Ser Val Glu Glu Ile Phe Asp Glu Phe Asp Thr Asp Gly Ser
340 345 350

Ala Thr Trp Ser Asp Arg Glu Val Arg Thr Phe Leu Thr Arg Ile Tyr
355 360 365

Gln Pro Pro Leu Asp Trp Ser Ala Met Arg Tyr Phe Glu Glu Val Val
370 375 380

Gln Asn Cys Thr Arg Asn Leu Gly Met His Leu Lys Val Asp Thr Val
385 390 395 400

Glu His Ser Thr Leu Val Tyr Glu Arg Tyr Glu Asp Ser Asn Leu Pro
405 410 415

Thr Ile Thr Arg Asp Leu Val Val Arg Cys Pro Leu Leu Ala Glu Ala
420 425 430

Leu Ala Ala Asn Phe Ala Val Arg Pro Lys Tyr Asn Phe His Val Ser
435 440 445

Pro Lys Arg Thr Ser His Ser Asn Phe Met Met Leu Thr Ser Asn Leu
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Thr Glu Val Val Glu Ser Leu Asp Arg Leu Arg Arg Asn Pro Arg Lys
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Glu Asp Gly Ala Pro Ser
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Arg Pro Ser Arg Asp Cys Ala Arg Val Arg Ser Gly Ser Pro Glu Gln
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Glu Ser Trp Pro Pro Pro Pro Leu Ala Thr His Glu Pro Arg Ala Pro
 35 40 45

Ser His His Ala Ala Val Arg Thr Phe Val Ser His Phe Glu Gly Arg
 50 55 60

Ala Val Ala Gly His Leu Thr Arg Val Ala Asp Pro Leu Arg Thr Phe
 65 70 75 80

Ser Val Leu Glu Pro Gly Gly Ala Gly Gly Cys Gly Gly Arg Ser Ala
 85 90 95

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<210> 24

<211> 6

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<213> Artificial Sequence

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Arg Ala Arg Tyr Lys Arg
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<210> 25

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<223> synthetic peptide

<400> 25

Pro Gly Ala Ala His Tyr
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<210> 26

<211> 46

<212> PRT

<213> Homo sapiens

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Lys Asn Thr Gly Arg Gln Leu Lys Asp Thr Phe Ala Asp Ser Leu Arg
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Tyr Val Asn Lys Ile Leu Asn Ser Lys Phe Gly Phe Thr Ser
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2009-12-01

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Arg Asp Thr Phe Ala Asp Ser Leu Arg
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<210> 35
<211> 25
<212> PRT
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<400> 35
Thr Gln Leu Ala Tyr Phe Thr Asp Ser Lys Asn Arg Ala Arg Tyr Lys
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Arg Asp Thr Phe Ala Asp Ser Leu Arg
20 25

<210> 36
<211> 75
<212> DNA
<213> hybrid

<400> 36
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gcagattccc tcaga

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<210> 37
<211> 25
<212> PRT
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<400> 37

Thr Gln Leu Ala Tyr Phe Thr Asp Ser Lys Asn Thr Asp Asp Asp Asp
1 5 10 15

Lys Asp Thr Phe Ala Asp Ser Leu Arg
20 25

<210> 38
<211> 25
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<213> hybrid

<400> 38

Thr Gln Leu Ala Tyr Phe Thr Asp Ser Lys Asn Pro Gly Ala Ala His
1 5 10 15

Tyr Asp Thr Phe Ala Asp Ser Leu Arg
20 25